```
============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2010; month=8; day=6; hr=7; min=56; sec=29; ms=677; ]
============================================================



*************************************************************
Reviewer Comments:
1.
A.
W112          Upper case found in data; Found at position(0) SeqId(1)
W112          Upper case found in data; Found at position(1) SeqId(1)
W112          Upper case found in data; Found at position(2) SeqId(1)
W112          Upper case found in data; Found at position(3) SeqId(1)
W112          Upper case found in data; Found at position(4) SeqId(1)
W112          Upper case found in data; Found at position(5) SeqId(1)
W112          Upper case found in data; Found at position(6) SeqId(1)
W112          Upper case found in data; Found at position(7) SeqId(1)
W112          Upper case found in data; Found at position(8) SeqId(1)
W112          Upper case found in data; Found at position(9) SeqId(1)
W112          Upper case found in data; Found at position(10) SeqId(1)
W112          Upper case found in data; Found at position(11) SeqId(1)
W112          Upper case found in data; Found at position(12) SeqId(1)
W112          Upper case found in data; Found at position(13) SeqId(1)
W112          Upper case found in data; Found at position(14) SeqId(1)
W112          Upper case found in data; Found at position(15) SeqId(1)
W112          Upper case found in data; Found at position(16) SeqId(1)
W112          Upper case found in data; Found at position(17) SeqId(1)
W112          Upper case found in data; Found at position(18) SeqId(1)
W112          Upper case found in data; Found at position(19) SeqId(1)
This error has occured more than 20 times, will not be displayed
W112          Upper case found in data; Found at position(0) SEQID(3)
W112          Upper case found in data; Found at position(1) SEQID(3)
W112          Upper case found in data; Found at position(2) SEQID(3)
W112          Upper case found in data; Found at position(3) SEQID(3)
W112          Upper case found in data; Found at position(4) SEQID(3)
W112          Upper case found in data; Found at position(5) SEQID(3)
```

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W112              Upper case found in data; Found at position(6)  SEQID(3)
W112              Upper case found in data; Found at position(7)  SEQID(3)
W112              Upper case found in data; Found at position(8)  SEQID(3)
W112              Upper case found in data; Found at position(9)  SEQID(3)
W112              Upper case found in data; Found at position(10) SEQID(3)
W112              Upper case found in data; Found at position(11) SEQID(3)
W112              Upper case found in data; Found at position(12) SEQID(3)
W112              Upper case found in data; Found at position(13) SEQID(3)
W112              Upper case found in data; Found at position(14) SEQID(3)
W112              Upper case found in data; Found at position(15) SEQID(3)
W112              Upper case found in data; Found at position(16) SEQID(3)
W112              Upper case found in data; Found at position(17) SEQID(3)
W112              Upper case found in data; Found at position(18) SEQID(3)
W112              Upper case found in data; Found at position(19) SEQID(3)
This error has occured more than 20 times, will not be displayed
W112              Upper case found in data; Found at position(0)  SEQID(8)
W112              Upper case found in data; Found at position(1)  SEQID(8)
W112              Upper case found in data; Found at position(2)  SEQID(8)
W112              Upper case found in data; Found at position(3)  SEQID(8)
W112              Upper case found in data; Found at position(4)  SEQID(8)
W112              Upper case found in data; Found at position(5)  SEQID(8)
W112              Upper case found in data; Found at position(6)  SEQID(8)
W112              Upper case found in data; Found at position(7)  SEQID(8)
W112              Upper case found in data; Found at position(8)  SEQID(8)
W112              Upper case found in data; Found at position(9)  SEQID(8)
W112              Upper case found in data; Found at position(10) SEQID(8)
W112              Upper case found in data; Found at position(11) SEQID(8)
W112              Upper case found in data; Found at position(12) SEQID(8)
W112              Upper case found in data; Found at position(13) SEQID(8)
W112              Upper case found in data; Found at position(14) SEQID(8)
W112              Upper case found in data; Found at position(15) SEQID(8)
W112              Upper case found in data; Found at position(16) SEQID(8)
W112              Upper case found in data; Found at position(17) SEQID(8)
W112              Upper case found in data; Found at position(18) SEQID(8)


W112              Upper case found in data; Found at position(19) SEQID(8)
This error has occured more than 20 times, will not be displayed


B.
E330              Invalid protein , found in SEQID(15) POS (1)Invalid
Protein:CGGGA
E330              Invalid protein , found in SEQID(15) POS (2)Invalid
```

Protein:TCCAT

E330   Invalid protein , found in SEQID(15) POS (3)Invalid
Protein:GCTGG

E330   Invalid protein , found in SEQID(15) POS (4)Invalid
Protein:ACAGC

E330   Invalid protein , found in SEQID(15) POS (5)Invalid
Protein:AACAA

E330   Invalid protein , found in SEQID(15) POS (6)Invalid
Protein:CAG

E330   Invalid protein , found in SEQID(29) POS (1)Invalid
Protein:TTTGA

E330   Invalid protein , found in SEQID(29) POS (2)Invalid
Protein:GCATT

E330   Invalid protein , found in SEQID(29) POS (3)Invalid
Protein:CTGGC

E330   Invalid protein , found in SEQID(29) POS (4)Invalid
Protein:TTC

E330   Invalid protein , found in SEQID(30) POS (1)Invalid
Protein:AAACA

E330   Invalid protein , found in SEQID(30) POS (2)Invalid
Protein:GAGCA

E330   Invalid protein , found in SEQID(30) POS (3)Invalid
Protein:GGTCC

E330   Invalid protein , found in SEQID(30) POS (4)Invalid
Protein:CGGCA

E330   Invalid protein , found in SEQID(30) POS (5)Invalid
Protein:GAAAT

E330   Invalid protein , found in SEQID(30) POS (6)Invalid
Protein:AGT

<210> 1
<211> 78
<212> DNA
<213> S. cerevisiae
<400> 1
GGAAT TCGGC ACCAT GTGCT TCTGT AAATA GTGTA TTGTG TTTTT AATGT 50
TGGAC TGGTT GGAAT AAAGC TCTAG AGC 78

A.
For SEQ ID # 1 through 21 and 23 through 30, "37 CFR 1.822 (c) Format
representation of nucleotides.(1) A nucleotide sequence shall be listed

using the lowercase letter for representing the one-letter code for the nucleotide bases set forth in WIPO Standard ST.25 (1998) Appendix 2, Table 1."
Please make all necessary changes.

B.
For SEQ ID # 1 through 21 and 23 through 30, nucleotide bases must be in groups of ten nucleotides, and maximum of 60 per line.

2.
A.
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (2)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (3)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (14)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (15)
E224   <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (16)

E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (17)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (18)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (19)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (20)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (21)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (22)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (23)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (24)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (25)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (26)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (27)
E224   <220>,<223> section required as <213> has Artificial
sequence or Unknown in SEQID (28) This error has occured more than 20
times, will not be displayed

B.
E254   The total number of bases conflicts with running total
Input: 0, Calculated : 27 SEQID(2)
E254   The total number of bases conflicts with running total
Input: 0, Calculated : 26 SEQID(3)
E254   The total number of bases conflicts with running total
Input: 0, Calculated : 21 SEQID(4)
E254   The total number of bases conflicts with running total
Input: 0, Calculated : 20 SEQID(5)
E254   The total number of bases conflicts with running total
Input: 0, Calculated : 24 SEQID(6)
E254   The total number of bases conflicts with running total
Input: 0, Calculated : 27 SEQID(7)
E254   The total number of bases conflicts with running total
Input: 0, Calculated : 26 SEQID(8)
E254   The total number of bases conflicts with running total

```
Input: 0, Calculated : 21 SEQID(9)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 24 SEQID(10)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 24 SEQID(11)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 21 SEQID(12)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 22 SEQID(13)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 35 SEQID(14)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 31 SEQID(16)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 26 SEQID(17)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 41 SEQID(18)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 41 SEQID(19)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 25 SEQID(20)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 24 SEQID(21)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 30 SEQID(23)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 21 SEQID(24)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 19 SEQID(25)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 24 SEQID(26)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 20 SEQID(27)
E254            The total number of bases conflicts with running total
Input: 0, Calculated : 17 SEQID(28)
E253            The number of bases differs from <211> Input: 28
Calculated:0 SEQID (15)
E253            The number of bases differs from <211> Input: 18
Calculated:0 SEQID (29)
E253            The number of bases differs from <211> Input: 28
Calculated:0 SEQID (30)
```

```
<210> 2
<211> 27
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia cDNA
<400> 2
GCGGA ATTCG TNSAR GTNAT HCCNT GG
```

A.

For SEQ ID # 1 through 30, the mandatory feature used to describe the source of the genetic material of an "Artificial sequence" should consist of both numeric identifier <220> and numeric identifier <223>. Numeric identifier "<220> feature" should remain blank, and numeric identifier "<223> Other Information" should provide "Other relevant information, four lines maximum." The mandatory numeric identifier <220> is missing from all of these sequences. Please add the mandatory numeric identifier <220>, between numeric identifier <213> and <223> in these sequences.

B.

For SEQ ID # 1 through 21 and 23 through 30, the sequence rules require that "the enumeration of nucleotide bases shall start at the first base of the sequence with 1. The enumeration shall be continuous through the whole sequence in the direction 5' to 3'. The enumeration shall be marked in the right margin, next to the line containing the one-letter codes for bases, and giving the number of the last base of that line." The enumeration is not marked in the right margin. Please add the enumeration in the right margin.

3.
E253   The number of bases differs from <211> Input: 17
Calculated: 0
SEQID(22)


```
<210>  22
<211>  17
```

```
<212>   PRT
<213>   Artificial sequence
<223>   C-terminal peptide of CPEB (CPEB77)


<400>   22


LCNSH QGNYF CRDLL CF
```

A.
For SEQ ID # 22, the sequence rules specify that amino acid must be shown using the "three-letter" abbreviations.

37 CFR
Sec. 1.822 Symbols and format to be used for nucleotide and/or amino acid sequence data.
(d) Representation of amino acids.
(1) The amino acids in a protein
or peptide sequence shall be listed using the three-letter abbreviation with the first letter as an upper case character, as in WIPO Standard ST.25 (1998), Appendix 2, Table 3.

Please change the amino acids to the correct "three-letter" abbreviations.

B.
37 CFR
Sec. 1.822 Symbols and format to be used for nucleotide and/or amino acid sequence data.
(d) Representation of amino acids.
(4) ...the enumeration of amino acids shall start at the first amino acid at the amino terminal as number 1. It shall be marked below the sequence every 5 amino acids.
Please number the amino acids according to the sequence rules.

4.
E253   The number of bases differs from <211> Input: 37
Calculated:35 SEQID (14)


```
<210>   14
<211>   37
```

```
<212>  DNA
<213>  Artificial sequence
<223>  Primer directed to Drosophila melanogaster cDNA


<400>  14


CCCTC GAGAA GCTTT TAACA CCAGC GAAAG GGGAC
```

For SEQ ID # 14, the number given for numeric identifier <211> must match the total number of bases found in the sequence. Numeric identifier <211> states there are 37 bases but, the total counted was 35. Please make all necessary changes.


```
5.
W402              Undefined organism found in <213> in SEQ ID (1)
W213              Artificial or Unknown found in <213> in SEQ ID (9)
W213              Artificial or Unknown found in <213> in SEQ ID (10)
W213              Artificial or Unknown found in <213> in SEQ ID (11)
W213              Artificial or Unknown found in <213> in SEQ ID (12)
W213              Artificial or Unknown found in <213> in SEQ ID (13)
W213              Artificial or Unknown found in <213> in SEQ ID (14)
W213              Artificial or Unknown found in <213> in SEQ ID (15)
W213              Artificial or Unknown found in <213> in SEQ ID (16)
W213              Artificial or Unknown found in <213> in SEQ ID (17)
W213              Artificial or Unknown found in <213> in SEQ ID (18)
W213              Artificial or Unknown found in <213> in SEQ ID (19)
W213              Artificial or Unknown found in <213> in SEQ ID (20)
W213              Artificial or Unknown found in <213> in SEQ ID (21)
W213              Artificial or Unknown found in <213> in SEQ ID (22)
W213              Artificial or Unknown found in <213> in SEQ ID (23)
W213              Artificial or Unknown found in <213> in SEQ ID (24)
W213              Artificial or Unknown found in <213> in SEQ ID (25)
W213              Artificial or Unknown found in <213> in SEQ ID (26)
W213              Artificial or Unknown found in <213> in SEQ ID (27)
W213              Artificial or Unknown found in <213> in SEQ ID (28) This
error has occured more than 20 times, will not be displayed
```

The warnings shown above are ok and require no response.
****

Application No: 10578203   Version No: 2.0

Input Set:

Output Set:

Started: 2010-07-23 15:40:38.370

Finished: 2010-07-23 15:41:08.364

Elapsed: 0 hr(s) 0 min(s) 29 sec(s) 994 ms

Total Warnings: 762

Total Errors: 75

No. of SeqIDs Defined: 30

Actual SeqID Count: 30

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 112	Upper case found in data; Found at position(0) SeqId(1)
W 112	Upper case found in data; Found at position(1) SeqId(1)
W 112	Upper case found in data; Found at position(2) SeqId(1)
W 112	Upper case found in data; Found at position(3) SeqId(1)
W 112	Upper case found in data; Found at position(4) SeqId(1)
W 112	Upper case found in data; Found at position(5) SeqId(1)
W 112	Upper case found in data; Found at position(6) SeqId(1)
W 112	Upper case found in data; Found at position(7) SeqId(1)
W 112	Upper case found in data; Found at position(8) SeqId(1)
W 112	Upper case found in data; Found at position(9) SeqId(1)
W 112	Upper case found in data; Found at position(10) SeqId(1)
W 112	Upper case found in data; Found at position(11) SeqId(1)
W 112	Upper case found in data; Found at position(12) SeqId(1)
W 112	Upper case found in data; Found at position(13) SeqId(1)
W 112	Upper case found in data; Found at position(14) SeqId(1)
W 112	Upper case found in data; Found at position(15) SeqId(1)
W 112	Upper case found in data; Found at position(16) SeqId(1)
W 112	Upper case found in data; Found at position(17) SeqId(1)
W 112	Upper case found in data; Found at position(18) SeqId(1)

```
        Input Set:


       Output Set:



           Started:   2010-07-23 15:40:38.370
          Finished:   2010-07-23 15:41:08.364
           Elapsed:   0 hr(s) 0 min(s) 29 sec(s) 994 ms
    Total Warnings:   762
      Total Errors:   75
No. of SeqIDs Defined:  30
   Actual SeqID Count:  30
```

Error code	Error Description
W 112	Upper case found in data; Found at position(19) SeqId(1) This error has occured more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (2)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 27 SEQID(2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (3)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 26 SEQID(3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 21 SEQID(4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 20 SEQID(5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)

```
              Input Set:


              Output Set:



              Started:    2010-07-23 15:40:38.370
             Finished:    2010-07-23 15:41:08.364
              Elapsed:    0 hr(s) 0 min(s) 29 sec(s) 994 ms
       Total Warnings:    762
         Total Errors:    75
No. of SeqIDs Defined:    30
    Actual SeqID Count:   30
```

Error code	Error Description
E 224	\<220\>,\<223\> section required as \<213\> has Artificial sequence or Unknown in SEQID (7)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 27 SEQID(7)
W 213	Artificial or Unknown found in \<213\> in SEQ ID (8)
E 224	\<220\>,\<223\> section required as \<213\> has Artificial sequence or Unknown in SEQID (8)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 26 SEQID(8)
W 213	Artificial or Unknown found in \<213\> in SEQ ID (9)
E 224	\<220\>,\<223\> section required as \<213\> has Artificial sequence or Unknown in SEQID (9)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 21 SEQID(9)
W 213	Artificial or Unknown found in \<213\> in SEQ ID (10)
E 224	\<220\>,\<223\> section required as \<213\> has Artificial sequence or Unknown in SEQID (10)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(10)
W 213	Artificial or Unknown found in \<213\> in SEQ ID (11)
E 224	\<220\>,\<223\> section required as \<213\> has Artificial sequence or Unknown in SEQID (11)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(11)
W 213	Artificial or Unknown found in \<213\> in SEQ ID (12)
E 224	\<220\>,\<223\> section required as \<213\> has Artificial sequence or Unknown in SEQID (12)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 21 SEQID(12)

Input Set:

Output Set:

Started:	2010-07-23 15:40:38.370
Finished:	2010-07-23 15:41:08.364
Elapsed:	0 hr(s) 0 min(s) 29 sec(s) 994 ms
Total Warnings:	762
Total Errors:	75
No. of SeqIDs Defined:	30
Actual SeqID Count:	30

Error code		Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (13)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
E	254	The total number of bases conflicts with running total Input: 0, Calculated : 22 SEQID(13)
W	213	Artificial or Unknown found in <213> in SEQ ID (14)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (14)
E	254	The total number of bases conflicts with running total Input: 0, Calculated : 35 SEQID(14)
E	253	The number of bases differs from <211> Input: 37 Calculated:35
W	213	Artificial or Unknown found in <213> in SEQ ID (15)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (15)
E	330	Invalid protein , found in SEQID(15) POS (1)Invalid Protein:CGGGA
E	330	Invalid protein , found in SEQID(15) POS (2)Invalid Protein:TCCAT
E	330	Invalid protein , found in SEQID(15) POS (3)Invalid Protein:GCTGG
E	330	Invalid protein , found in SEQID(15) POS (4)Invalid Protein:ACAGC
E	330	Invalid protein , found in SEQID(15) POS (5)Invalid Protein:AACAA
E	330	Invalid protein , found in SEQID(15) POS (6)Invalid Protein:CAG
E	253	The number of bases differs from <211> Input: 28 Calculated:0
W	213	Artificial or Unknown found in <213> in SEQ ID (16)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (16)
E	254	The total number of bases conflicts with running total Input: 0, Calculated : 31 SEQID(16)

Input Set:

Output Set:

Started: 2010-07-23 15:40:38.370
Finished: 2010-07-23 15:41:08.364
Elapsed: 0 hr(s) 0 min(s) 29 sec(s) 994 ms
Total Warnings: 762
Total Errors: 75
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (17)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 26 SEQID(17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (18)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 41 SEQID(18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (19)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 41 SEQID(19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 25 SEQID(20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21) This error has occured more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (21) This error has occured more than 20 times, will not be displayed
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(21)
E 331	Count of Protein differs from the <211> tag Input: 17
E 254	The total number of bases conflicts with running total Input: 0,

```
                   Input Set:


                   Output Set:



               Started:  2010-07-23 15:40:38.370
              Finished:  2010-07-23 15:41:08.364
               Elapsed:  0 hr(s) 0 min(s) 29 sec(s) 994 ms
        Total Warnings:  762
          Total Errors:  75
   No. of SeqIDs Defined:  30
     Actual SeqID Count:   30
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Error code   Error Description

               This error has occured more than 20 times, will not be displayed

E   330   Invalid protein , found in SEQID(29) POS (1)Invalid Protein:TTTGA

E   330   Invalid protein , found in SEQID(29) POS (2)Invalid Protein:GCATT

E   330   Invalid protein , found in SEQID(29) POS (3)Invalid Protein:CTGGC

E   330   Invalid protein , found in SEQID(29) POS (4)Invalid Protein:TTC

E   253   The number of bases differs from <211> Input: 18 Calculated:0

E   330   Invalid protein , found in SEQID(30) POS (1)Invalid Protein:AAACA

E   330   Invalid protein , found in SEQID(30) POS (2)Invalid Protein:GAGCA

E   330   Invalid protein , found in SEQID(30) POS (3)Invalid Protein:GGTCC

E   330   Invalid protein , found in SEQID(30) POS (4)Invalid Protein:CGGCA

E   330   Invalid protein , found in SEQID(30) POS (5)Invalid Protein:GAAAT

E   330   Invalid protein , found in SEQID(30) POS (6)Invalid Protein:AGT

E   253   The number of bases differs from <211> Input: 28 Calculated:0

<110>   Kausik Si and Eric Kandel

<120>   Prion-like form of CPEB and related compositions and methods

<130>   68103/JPW/BJA

<140>   10578203
<141>   2010-07-23

<150>   PCT/US04/36781
<151>   2004-11-05

<150>   60/518,385
<151>   2003-11-07

<160>   30

<170>   PatentIn version 3.3

<210>   1
<211>   78
<212>   DNA
<213>   S. cerevisiae

<400>   1

GGAAT TCGGC ACCAT GTGCT TCTGT AAATA GTGTA TTGTG TTTTT AATGT   50
TGGAC TGGTT GGAAT AAAGC TCTAG AGC   78

<210>   2
<211>   27
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Aplysia cDNA

<400>   2

GCGGA ATTCG TNSAR GTNAT HCCNT GG

<210>   3
<211>   26
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Aplysia cDNA

<400>   3

GCGGG ATCCT GNTGC CANTS CCARC A

<210> 4
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia mRNA

<400> 4

CACTG TCTTG TTCGA CTCCA G

<210> 5
<211> 20
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia mRNA
<400> 5

AACAC ATGGT TACTG TCCGC

<210> 6
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia mRNA

<400> 6

CATGA AAGCC GTGCA AGCTG CATT

<210> 7
<211> 27
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA and cDNA

<400> 7

CGGGA TCCAT GTACA ACAAA TTTGT TA

<210> 8
<211> 26
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 8

TCCCC GCGGC GATCC TCCGC CTCCT C

<210> 9
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 9

ATGGA CTCGC TCAAG TTACC A

<210> 10
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 10

CGCGA TGCCT GATTG ATTGT TGAA

<210> 11
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 11

TGTGC GTTAT TTTAT CGTTT AGTG

<210> 12
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 12

GACTT CATCC GCCAC CAGTC G

<210> 13
<211> 22
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 13

CACCA GGAAC TTCTT GAATC CG

<210>   14
<211>   37
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Drosophila melanogaster cDNA

<400>   14

CCCTC GAGAA GCTTT TAACA CCAGC GAAAG GGGAC

<210>   15
<211>   28
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Drosophila melanogaster cDNA

<400>   15

CGGGA TCCAT GCTGG ACAGC AACAA CAG

<210>   16
<211>   31
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Drosophila melanogaster cDNA

<400>   16

GACTA GTCTA GAATA GATTA GCAAA GAAAT C

<210>   17
<211>   26
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Aplysia neuronal actin cDNA

<400>   17

GGGAA TTCGT CTGGA GCCAC CAACA C

<210>   18
<211>   41
<212>   DNA
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<223>   Primer directed to Aplysia neuronal actin

<400>   18

CGGAT CCATT TATTA ACATT GTATA AAAAA TACAG TTGAA C

<210>   19
<211>   41
<212>   DNA
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<400>   19

CGGAT CCATT TATTA ACATT GTATG GGAAA TACAG TTGAA C

<210>   20
<211>   25
<212>   DNA
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<223>   Primer directed to Aplysia CPEB cDNA

<400>   20

CGGGA TCCAT GCAAG CCATG GCCGT

<210>   21
<211>   24
<212>   DNA
<213>   Artificial sequence
<223>   Primer directed to Aplysia CPEB cDNA

<400>   21

TCCCC GCGGT GGACC AGGCG TGTA

<210>   22
<211>   17
<212>   PRT
<213>   Artificial sequence
<223>   C-terminal peptide of CPEB (CPEB77)

<400>   22

LCNSH QGNYF CRDLL CF

<210>   23

<211> 30
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia RNA

<400> 23

GCGAG CTCCG CGGCC GCGTT TTTTT TTTTT

<210> 24
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia sensorin RNA

<400> 24

AACAG AAACA GTCTT TCCCC C

<210> 25
<211> 19
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia sensorin RNA

<400> 25

TCTTG ACTCA CCAAC TGCC

<210> 26
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia Bmp1 RNA

<400> 26

ATCTA TCGCC TATTA TTATC ACCA

<210> 27
<211> 20
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia Bmp1 RNA

<400> 27

ATCCC ATGCA TTTGT TTGTT

<210> 28
<211> 17
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia N-actin RNA

<400> 28

CCCAT CCATT GTCCA CA

<210> 29
<211> 18
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia N-actin RNA

<400> 29

TTTGA GCATT CTGGC TTC

<210> 30
<211> 28
<212> DNA
<213> Artificial sequence
<223> Antisense oilgo directed to Aplysia CPEB mRNA

<400> 30

AAACA GAGCA GGTCC CGGCA GAAAT AGT